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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Peptide #2054 enco	AAM15620	22	118	90.8	276	10
Human bone marrow	AAM67811	22	118	90.8	276	ø
Human brain expres	AAM55415	22	118	90.8	276	8
Protein #2034 enco	ABB20035	22	118	90.8	276	7
Peptide #2131 enco	ABB34625	22	118	90.8	276	თ
Peptide #2100 enco	ABB29449	22	118	90.8	276	v
Human cancer assoc	AAB43549	21	170	100.0	304	4
Human ovarian anti	ABP42408	23	66	100.0	304	w
Antimicrobial pept	AAW95381	20	59	100.0	304	N
Heparin-binding pr	AAR48204	15	59	100.0	304	1
Description	ID	:	Query Match Length DB	Query Match	Score	Result

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123.5	163	168.5	175	175	188.5	201	208	208	208	211	211.5	231	231	231	231	231	231	238	238	238	238	239	239	239	239	239	239	239	239	239	263	276	276	276
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ABG34132	AAO07113	AAU30219	ABG27520	ABG27230	AAB18318	AAO08731	ABG27519	ABG27228	AAW03681	AAG75965	AAU30872	AAG31871	AAG48690	AAG39476	AAG38861	AAG15348	AAG04311	AAG01569	AAG4 0703	AAG40788	AAG40704	AAG26728	AAG32886	AAG34118	AAG32887	AAG44882	AAG44883	AAG34119		AAG22753	ABB70963	ABG37354	336	AAM28118
	Human polypeptide	Novel human secret	human	Novel human diagno	Plasmodium falcipa	Human polypeptide	1 human		Long term potentia	Human colon cancer	весте	thali	thali	Arabidopsis thalia	$\boldsymbol{\sigma}$	Arabidopsis thalia	~	Human secreted pro	mays prot	maya prot	mays prot	mays	mays prot	ea mays prot	hila me	n peptide	ptide #2046 enc	N						

## ALIGNMENTS

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a cell growth agent and in the treatment of wounds and bone disease		Claim 1; Page 3; 4pp; Japanese.		disease	New heparin-binding protein - used as a cell growth agent for		WPI; 1994-031824/04.		(FARH ) HOECHST JAPAN LTD.		05-JUN-1992; 92JP-0145125.		05-JUN-1992; 92JP-0145125.		21-DEC-1993.		JP05339287-A.		Rattus norvegicus.		Cell growth agent; wound; bone disease; treatment; treating; agent.		Heparin-binding protein.		12-JUL-1994 (first entry)		AAR48204;		AAR48204 standard; protein; 59 AA.	ET: 1 8204	

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                                                                                                                                                                                                                                                                                                                                                      Ubiquicidine, treatment, diagnosis, prophylaxis, infection, microbial, pathogenic, Gram-positive bacteria, antimicrobial, Staphylococcus aureus, Listeria monocytogenes, Gram-negative, Klebsiella pneumoniae, E. coli, enterococcus, Salmonella typhinuriom, Mycobacterium avium, M. fortuium, fungus, Candida albicans, Cryptococcus neoformans, Aspergillus fumigatis, virus, parasite, Trypanosoma cruzi, Taxoplasma gondii.
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antimicrobial peptides derived from ubiquicidine - useful for the prophylaxis, diagnosis and treatment of infections in humans and animals
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                                                                                                  1 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS
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                             100.0%; Score 304; DB 15;
100.0%; Pred. No. 2.5e-32;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 23; 48pp; English.
                                                                                                                                                                                                                      AAW95381 standard; peptide; 59
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                                                                                                                                                                                                                                                                                       (first entry)
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                                                                 59; Conservative
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                                                 Best Local Similarity
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to polynucleotides, antibodies against human ovarian antigens and the use of ovarian antigen polynucleotides and polypeptides in diagnosing.

Creating, prognosing or preventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), candinate disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and urinary system antigen expression or activity. The polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the
                                                                                                                                                                                                                                                                                                                                               Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytoscatic; immunomodulatory; neuroprotective; antiinflammatory; synaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                            59
                      KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS
1 KVHGSLARAGKVRGQTPKVAKQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS
                                                                                                                                                                                                                                                                                                          Human ovarian antigen HOCMY79, SEQ ID NO:3540.
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                                                                                                                                                               ABP42408 standard; Protein; 66
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                                                                                                                                                                                                                                                         (first entry)
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RESULT 4
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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB33398 to AAB4239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antivinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarrhritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant, nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; haematopoietic cell disorder; autoimmune disorder; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENOME SCI INC
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Pred. No. 2.8e-32;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen; detection;
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far great
                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; microarray; single exon probe; gene disease; cancer.
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                                                                                                                                                                                                                                   useful
                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2000;
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                                                                                                                                                                                                                                                                              2001-496933/54
                                                                                                                                                                                                                                                                                                            SG,
                                                                                                                                                                                      27;
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                                                                                                                                                                                                                                                                                                                                          MOLECULAR DYNAMICS INC
                                                                                                                                                                                       SEQ
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; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
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                                                                                                                                                                                       ID NO
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                                                                                                                                                                                       12417;
                                                                                                                                                                                                                                                                                                            Chen W,
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Pred. No. 8.1e-32;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                            Rank DR
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presents a far greater

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Sequence
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences.
diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for repid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                              probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                        56 KVHGSLARAGKVRGQTPKVAKQEKKKKKKKKTGQATRRMQYNRRFVNVVPTFSKKKGPN 115
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                            1 KVHGSLARAGKVRGQTPKVAKQEKK----KKKTGRAKRRMQYNRRFVNVVPTFGKKKGPN 56
                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                             Peptide #2131 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 27260; 639pp + sequence listing; English.
                                                                                                                          Score 276, DB 22; Length 118;
Pred. No. 2.5e-28;
1; Mismatches 2; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid I
analyzing gene expression in human fetal liver
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                                                                                                                                                                                                                                                                                                        ABB34625 standard; Peptide; 118 AA.
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26-MAY-2000; 2000US-0207456.
30-UJN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0224687.
27-SEP-2000; 2000US-023687.
04-OCT-2000; 2000GB-0024263.
                                                                                                                             90.8%;
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                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                      Conservative
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                                                                                                                                        Best Local Similarity
Matches 56; Conserv
                                                                                                         118 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                 ABB34625;
                                                                                                        Sequence
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                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein #2034 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                         KVHGSLARAGKVRGQTPKVAKQEKKKKRRKKTGQATRRMQYNRRFVNVVPTPSKKKGPN 115
                                                             Gaps
                                                                                                          1 KVHGSLARAGKVRGQTPKVAKQEKK----KKKTGRAKRRMQYNRRFVNVVPTFGKKKGPN 56
                                                             4,
     Length 118;
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Pred. No. 2.5e-28;
  , DB 22;
2.5e-28;
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                                                        1; Mismatches
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90.8%; Score 276;
                              Pred. No.
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26-MAY-2000; 2000US-0207456.
30-UJN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000US-024263.
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                         88.98;
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                                                        56; Conservative
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                                                                                                                                                                                                                                                                        ANS 118
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                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human brain expressed single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-2001
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116
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                                                                                                                                                                                                                   Local Similarity
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ANS
                                                                                       ANS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVHGSLARAGKVRGQTPKVAKQEKKKKKRKKKTGQATRRMQYNRRFVNVVPTFSKKKGPN 115
                                           SNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULAR DYNAMICS INC
                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                            of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO: 27520; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312
2000US-0207456
2000US-0608408
2000US-0632366
2000US-0632366
2000US-0234369
2000US-0236359
2000US-0236359
                                                                                                                                                                                         90.8%;
ilarity 88.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.
                                                                                                                                                                                         Score 276; DB 22;
Pred. No. 2.5e-28;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon probe encoded protein SEQ ID NO: 27520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                          Length 118;
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RESULT 10
AAM15620
ID AAM15
XX
AC AAM15
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XX
DE Pepti
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AAM67811
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Best Local S
Matches 56
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26-MAY-2000; 2000US-020456.
30-JUN-20000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234639.
04-OCT-2000; 2000US-0234639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                AAM15620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO: 28117; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001
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  Peptide #2054 encoded by probe for measuring cervical gene expression.
                                                         12-OCT-2001
                                                                                                                                                                       AAM15620 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn
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                                                                                                                                                                                                                                                                                                           116 ANS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                      2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                  ANS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome-derived single exon nucleic acid probes useful zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.8%;
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                                                                                                                                                                       118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 276; DB 22;
Pred. No. 2.5e-28;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probe encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 KVHGSLARAGKVRGQTPKVAKQEKKKKKKKKKKTGQATRRMQYNRFVNVVPTFSKKKGPN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KVHGSLARAGKVRGQTPKVAKQEKK----KKKTGRAKRRMQYNRRFVNVVPTFGKKKGPN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #2046 encoded by probe for measuring breast gene expression
                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                             analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID No 28387; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM03364 standard; Protein; 118 AA
                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-UJN-2000; 2000US-06034.08.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
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26-MAY-2000; 2000US-0207456.
30-UUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
                                                                            30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2001; 2001WO-US00661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human genetic disorders.
                                                                                                                                                                                                                                                                                                                Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 AA;
WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157270-A2
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                                      09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Best Local 3
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H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #2155 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVHGSLARAGKVRGQTPKVAKQEKKKKKKKKKKKTGQATRRMQYNRRFVNVVPTFSKKKGPN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KVHGSLARAGKVRGQTPKVAKQEKK----KKKTGRAKRRMQYNRRFVNVVPTFGKKKGPN 56
                  microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.8%; Score 276; DB 22;
88.9%; Pred. No. 2.5e-28;
iive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID No 20446; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM28118 standard; Protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                    26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                            30-JAN-2001; 2001WO-US00670
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                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 AA;
                                        cervical cancer
                                                                                                                  WO200157278-A2
                                                                              Homo sapiens
                                                                                                                                                                                                                                  04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 ANS 59
                                                                                                                                                        09-AUG-2001
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Gaps

2; Indels

Score 276; DB 22; Pred. No. 2.5e-28;

Rank

1; Mismatches

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RESULT 13
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ID ABG37
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                                                                                                                                                                          chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; nurrofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for nucleic acid expressed in the human breast. The probes are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG37354 standard; Peptide; 118 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form specification, but was obtained in electronic format
04-FEB-2000; 2000US-180312P
26-MAY-2000; 2000US-207456P
                                                                                                                                                                                                                                                                                                                                        Human peptide
                                                                                                                                                                                                                                                                                                                                                                           19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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04-OCT-2000;
                                               30-JAN-2001; 2001WO-US00665
                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 KVHGSLARAGKVRGQTPKVAKQEKKKKKKKKTGQATRRMQYNRRFVNVVPTFSKKKGPN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KVHGSLARAGKVRGQTPKVAKQEKK----KKKTGRAKRRMQYNRRFVNVVPTFGKKKGPN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; SEQ ID No 12104; 322pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                    encoded by genome-derived single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 276;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                        SEQ ID 27019
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116 ANS 118

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                                                                                                                                                                                                                                                                                       Ct tissues and/or cell types using hybridisation to a single exon common pattern of cexpression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one common pattern of the exons should be assigned to a single gene; a peptide comprising one compression of the exons should be assigned to a single gene; a peptide comprising one compression analysis, and for the specification, or encoded by the compression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases (COpp), interstitial lung disease (ILD), familial idiopathic pulmonary disease (COpp), interstitial lung disease (ILD), familial idiopathic pulmonary (fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, commonary disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary (pulmonary disease, tuberous sclerosis, Gaucher's disease, commonary disease, primary ciliary dyskinesis, pulmonary hypertension commonary disease, primary ciliary dyskinesis, pulmonary hypertension commonary disease. The present sequence is a peptide/protein commonated by a single exon probe of the invention.

CC note: The sequence data for this patent did not form part commonate in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC probes: Also included are a microarray comprising the novel set of corprobes; the novel set of probes which hybridise at high stringency to a collectic acid expressed in the human lung; measuring gene expression in a collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with care collection of detectably labeled nucleic acids derived from human lung companies are comprising (a) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising companies sequences (a) algorithmically predicting at least one exon from genomic sequences (b) the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several
                                                                                                                                      Query Match
Best Local S
Matches 56
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 nucleic acid sequences.
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn
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                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
    57
                                                 56
                                                                         1 KVHGSLARAGKVRGQTPKVAKQEKK----KKKTGRAKRRMQYNRRFVNVVPTFGKKKGPN 56
    SNA
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                                                 KVHGŚLARAGKVRGQTPKVAKQEKKKKKKKKKTGQATRRMQYNRRFVNVVPTFSKKKGPN 115
                                                                                                                                                            Similarity
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    59
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2000US-0632366.
2000US-234687P.
2000US-236359P.
2000US-236359P.
                                                                                                                                         Conservative
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                                                                                                                                                         90.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in human
                                                                                                                                    Score 276; DB
Pred. No. 2.5e
1; Mismatches
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                                                                                                                             DB 23;
2.5e-28;
2;
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99US-0128714
99US-0128714
99US-0130449
99US-01304049
99US-01308510
99US-0131449
99US-0132407
99US-0132485
99US-0132485
99US-0132485
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99US-0132487
99US-0132487
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99US-0132487
99US-013428
99US-0134219
99US-0134219
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990S-0139453.
990S-0139492.
990S-0139455.
990S-0139456.
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99US-0126785.
99US-0127462.
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99US-0137502.
99US-0137724.
99US-0138094.
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99US-0138847.
99US-0139119.
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99US-0140823
              Zea mays subsp. mays.
                                                EP1033405-A2
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28-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 39681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays protein fragment SEQ ID NO: 25803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li PWD, Myers EW;
                                ABB70963 standard; Protein; 132 AA.
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                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                 26-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50; Conservative
                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY.
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Matches 50, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 132 AA;
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                                                                                                                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interactions -
                                                                                                                                                                                                                                                                                              27-SEP-2001
                                                                   ABB70963;
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                ABB70963
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3-0142055 3-0142390 3-0142803 3-0142920 3-0142977 3-0143542 3-0143624

-0140991. -0141287. -0141842.

22

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Query Ma
Best Loc
Matches
                                             13-SEP 1999
16-SEP 1999
27-SEP 1999
28-SEP 1999
28-SEP 1999
29-SEP 1999
29-SEP 1999
29-SEP 1999
29-SEP 1999
20-OCT 1999
11-OCT 1999
            y Match
Local
ch 78.6%;
l Similarity 79.3%;
46; Conservative
                                             99US-0153758
99US-0154019
99US-0155139
99US-0155486
99US-0155486
99US-0155486
99US-0155486
99US-0155486
99US-0155486
99US-0156596
99US-0159294
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99US-0159637
99US-0160767
99US-0160767
99US-0160768
99US-0160814
99US-0160814
99US-0161405
Score 239; DB 21;
Pred. No. 8.4e-24;
5; Mismatches 7;
                       Length
   Indels
                         62;
  0
   Gaps
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29-JUN-1999
01-JUL-1999
01-JUL-1999
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01-JUL-1999
02-JUL-1999
03-JUL-1999
03-JUL-1999
03-JUL-1999
04-JUL-1999
05-JUL-1999
07-JUL-1999
08-JUL-1999
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### ALIGNMENTS

ubiquitin-like protein / ribosomal protein S30, cytosolic [validated] - rat N;Contains: ribosomal protein S30; ubiquitin-like protein C;Species: Rattus norvegicus (Norway rat) C;Date: 21-Jul-2000 #sequence revision 21-Jul-2000 #text\_change 21-Jul-2000 C;Accession: A47416; B47416; S18101 R;Olvera, J; Wool, I.G.

A;Cross references: EMBL:X62671; NID:g407165; PIDN:CAA44545.1; PID:g57566
A;Accession: B47416
A;Molecule type: protein
A;Residues: 75-92 <012>
A;Note: the proteins are designated as ubiquitin-like protein and ribosomal protein S30 C;Superfamily: ubiquitin-like protein / rat ribosomal protein S30; ubiquitin homology C;Superfamily: ubiquitin-like protein #status predicted <UBI>F;1-74/Product: ubiquitin-like protein #status predicted <UBI>F;1-74/Domain: ubiquitin homology <UBH-F;75-133/Product: ribosomal protein S30 #status experimental <RIB> A; Molecule type: DNA
A; Residues: 1-133 < KAS>
A; Cross references: EMBL:X65921; NID:g31304; PIDN:CAA46714.1; PID:g31305
A; Cross references: EMBL:X65921; NID:g31304; PIDN:CAA46714.1; PID:g31305
A; Cross references: EMBL:X65921; NID:g31304; PIDN:CAA46714.1; PID:g31305
A; Michiels, L.; Van der Rauwelaert, E.; Van Hasselt, F.; Kas, K.; Merregu
Oncogene 8, 2537-2546, 1993
Oncogene 8, 2537-2546, 1993 ubiquitin-like protein / ribosomal protein S30, cytosolic - human N;Alternate names: fau protein (c;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text\_change 24-Sep-1999 C;Accession: JC1278; 137387; \$68911; \$21449; \$21450 C;Accession: JC1278; 137387; \$68911; \$21449; \$21450 C;Accession: JChiels, L.; Merregaert, J. Blochem. Biophys. Res. Commun. 187, 927-933, 1992 A;Title: Genomic structure and expression of the human fau gene: Encoding the A;Reference number: JC1278; MUID:92412144; PMID:1326960 A;Accession: JC1278 RESULT 2 JC1278 R;Olvera, J.; Wool, I.G.
J. Biol. Chem. 268, 17967-17974, 1993
A;Title: The carboxyl extension of a ubiquitin-like protein is rat ribosomal protein S30.
A;Reference number: A47416; MUID:93352612; PMID:8394356
A;Accession: A47416. á 밁 A; Molecule type: mRNA A; Residues: 1-133 <OLV> Matches Query Match 75 Local 1 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 133 Similarity 100 59; Conservative 100.0%; Score 304; DB 1; 100.0%; Pred. No. 2.8e-25; htive 0; Mismatches 0; Length 133; Indels <u>..</u> Merregaert, the ribosomal 0 4

Oncogene 8, 2 A; Title: fau

cDNA encodes a ubiquitin-like-S30 fusion protein and is expressed as an

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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, I. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
Aftile: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                      FIBOSONAL PROTEIN S30 homolog [imported] - Arabidopsis thaliana C'Species: Arabidopsis thaliana (mouse-ear cress) C'Species: Arabidopsis thaliana (mouse-ear cress) C'Species: Arabidopsis thaliana (mouse-ear cress) Hext_change 16-Feb-2001 (C')Accession: H85342 The European Union Arabidopsis Genome Sequencing Consortium, The ColNature 402, 769-777, 1999 A'Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A'Reference number: A85001; MUID:20083488; PMID:10617198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:NC_001268; NID:97269837; PIDN:CAB79697.1; GSPDB:GN00140
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Cipare: 20-85p-1999 #sequence_revision 20-8ep-1999 #text_change 24-Nov-1999
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Rigeisel, C.; Stellyes, L.; Bradshaw, H.
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A;Molecule type: DNA
A;Residues: 1-68 <STO>
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A;Map position: 4
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               A,Molecule type: mRNA
A;Residues: 1-133 «RES-
A;Cross-references: EMBL:X65923; NID:g31302; PIDN:CAA46716.1; PID:g31303
A;Cross-references: EMBL:X65923; NID:g31302; PIDN:CAA46716.1; PID:g31303
R;Vladimirov, S.N.; Ivanov, A.V.; Karpova, G.G.; Musolyamov, A.K.; Egorov, T.A.; Thiede, Bx;Vladimirov, S.N.; Ivanov, A.V.; Karpova, G.G.; Musolyamov, A.K.; Egorov, T.A.; Thiede, A;Title: Characterization of the human small-ribosomal-subunit proteins by N-terminal an A;Reference number: S68911
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 75-99 «VLA»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NiAlternate names: gene fau protein; monoclonal nonspecific suppressor factor beta C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 12-Aug-1996 #sequence revision 13936 #s. 21452
R; Michiels, L.; Van der Rauwelaert, E.; Van Hasselt, F.; Kas, K.; Merregaert, J.
Oncogene 8, 2537-2546, 1993
A; Title: fau CDNA encodes a ubiquitin-like-S30 fusion protein and is expressed as an ant A; Reference number: 137387; MUID: 93368957; PMID: 8395683
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A;Residues: 1-133 <CAS.
A;Cross-references: GB:L33715; NID:g497610; PIDN:AAA91564.1; PID:g497611
A;Cross-references: GB:L33715; NID:g497610; PIDN:AAA91564.1; PID:g497611
A;Note: authors translated the codon GTT for residue 119 as Arg, and GTC for residue 120
R;Nakamura, M.; Xavier, R.M.; Tsunematsu, T.; Tanigawa, Y.
Proc. Natl. Acad. Sci. U.S.A. 92, 3463-3467, 1995
A;Title: Molecular cloning and characterization of a cDNA encoding monoclonal nonspecifi
A;Reference number: I59368; MUID:95241522; PMID:7724584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: mRNÅ
A,Rebidues: 1-13] «RES.
A,Krebidues: 1-13] «RES.
A,Cross-references: EMBL:X65922, NID:950949; PIDN:CAA46715.1; PID:950950
R,Casteels, D.; Poirier, C.; Guenet, J.L.; Merregaert, J.
R,Casteels, D.; Poirier, C.; Guenet, J.L.; Merregaert, A.
A,Title: The mouse Fau gene: genomic structure, chromosomal localization, and characteri
A,Reference number: A56532; MUID:95293388; PMID:7774934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KVHGSLARAGKVRGQTPKVAKQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology C;Reywords: procein blosynthesis; ribosome F:1-74/Domain: ubiquitin homology (UBH>) F:1-74/Domain: ubiquitin homology (UBH>) F:75-133/Product: ribosomal protein S30, cytosolic #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology;1-74/Domain: ubiquitin homology <UBH>
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number: 137387; MUID:93368957; PMID:8395683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 304; DB 2;
100.0%; Pred. No. 2.8e-25;
ive 0; Mismatches 0;
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Pred, No. 2.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ribosomal protein fau - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 25/3; 74/1; 92/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Introns: 25/3; 74/1; 92/3
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Best Local Similarity
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A; Status: preliminary
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Query Match

A;Gene: fau

Best Local

75

g ò

RESULT 3

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ribosomal protein s30 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C;Accession: T39834
R;Lyne, M.; Rajandream. M A . D. D. Dec-1999 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 13-Aug-1999 (;Accession: A71604 R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O. Science 282, 1126-1132, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 5
A;Introns: 27/3; 71/1
C;Superfamily: unassi
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C;Superfamily: yeast ribosomal protein S30.e
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A;Experimental source: strain Bristol N2; clone C26F1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-130 <GEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: The sequence
A;Map
                      A; Gene: SPDB:SPBC19G7.03c
                                                             A;Residues: 1-61 <LYN>
A;Residues: 1-61 <LYN>
A;Cross-references: EMBL:AL021839; PIDN:CAA17057.2; GSPDB:GN00067;
A;Experimental source: strain 972h-; cosmid c19G7
                                                                                                                               A; Molecule type: DNA
                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                         A;Reference number: Z21884
A;Accession: T39834
                                                                                                                                                                                             submitted to the EMBL Data Library, February 1998
A;Reference number: Z21884
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A; Residues: 1-58 < GAR >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum A;Reference number: A71600; MUID:99021743; PMID:9804551 A;Accession: A71604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ribosomal protein S30 PFB0885w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: GB:AE001422;
Experimental source: clone 3D7;
                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity 64.4
38; Conservative
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Pred. No. 2.4e
8; Mismatches
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Pred. No. 4e-17;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4e-13;
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                                                                                    SPDB:SPBC19G7.03c
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RESULT
S38383
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A;Title: The yeast homolog of mammalian ribosomal protein A;Reference number: S70774; MUID:96278780; PMID:8662789
A;Accession: S70775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
S67074
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
C;Accession: S38383
                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: yeast ribosomal protein S30.e
C;Keywords: cytosol; protein biosynthesis; ribosome
F;2-63/Product: ribosomal protein S30.e, cytosolic #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribosomal protein S30.e, cytosolic - yeast (Saccharomyces cerevisiae) N;Alternate names: protein O4725; protein YLR287c-a; protein YOR182c C;Species: Saccharomyces cerevisiae
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A; Residues: 1-63 < BAK>
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                                                               SEB4B protein - human (fragment)
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A;Cross-references: MIPS:YLR287c-a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: SGD:RPS30B; MIPS:YOR182c
A;Cross-references: MIPS:YOR182c;
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A; Residues: 2-63 < BA3 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U48699; NID:g1256750; PIDN:AAC49316.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-63 <BAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 12R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics: <YS30A>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 1/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S70776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Genetics: YS30A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U48700; NID:g1256752; PIDN:AAC49317.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-63 <HUG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics: <YS30B>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                      1 KVHGSLARAGKVRGQTEKVAKQEKKKKKTGRAKRRMQYNRREVNVVPTFGKKK---GPN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVHGSLARAGKVKSOTPKVEKQEKPKQPKGRAYKRLLYVRRFVNVTNMVGGKRRMNPSS
                                                                                                                                                                               KVHGSLARAGKVKSQTPKVEKTEKPKKPKGRAYKRLLYTRRFVNVTLVNGKRRMNPGPS
                                                                                                                                                                                                                                                                        Similarity
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37; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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ce: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.9%;
62.7%;
                                                                                                                                                                                                                                                                                           57.7%;
62.7%;
                                                                                                                                                                                                                                                                      Score 175.5; DB 1;
Pred. No. 6.2e-12;
6; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 176; DB 2;
Pred. No. 5.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGD: S0005708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGD:S0004278
                                                                                                                                                                                                                                                                                                                DB 1;
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Tibosomal protein L4 - Mycoplasma pneumoniae (strain ATCC 29342)
N:Alternate names: hypothetical protein VXpSPT7_orf212
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C;Accession: S73991
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Mucleic Acids Res. 24, 4420-449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumonia A;Reference number: S73327; MUD:97105885; PMID:8948633
A;Accession: S73991
A;Scatus: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-212 <HIM*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleocapsid protein - murine hepatitis virus (strain A59)
C;Species: murine hepatitis virus, MHV
A;Variety: strain A59
A;Variety: strain A59
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: A45340; A04023; Ā47310
B;Parker, M.M.; Masters, P.S.
Virology 179, 463-468, 1990
A;Title: Sequence comparison of the N genes of five strains of the coronavirus mouse here.
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A,Residues: 1-108,'AVLLKHLMGSRSNYCPDGIFTILAQGPMLEPVMETALKES','SGLQTAKRTPIPALILSKGTQAVMR
A,Cross-references: GB:X00509; GB:J02252; NID:958965
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Virology 196, 196, 1973
A;Title: Evidence for new transcriptional units encoded at the 3' end of the mouse heparally. Reference number: A47310; MUID:93362405; PMID:8395114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AE000061, GB:U00089; NID:g1674336; PIDN:AAB96313.1; PID:g16743
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
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A;Residues: 1-454 <PAR>
A;Residues: 1-454 <PAR>
A;Cross-references: GB:M35256; NID:g331826; PIDN:AAA46447.1; PID:g331827
R;Armstrong, J.; Smeekens, S.; Rottier, P.
Nucleic Acids Res. 11, 883-891, 1983
A;Title: Sequence of the nucleocapsid gene from murine coronavirus MHV-A59.
A;Reference number: A04023; MUID:83168908; PMID:6687635
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A;Residues: 301-454 <SCH>
A;Cross-references: GB:864884; NID:g408334; PIDN:AAB27902.1; PID:g408335
A;Note: sequence extracted from NCBI backbone (NCBIN:136580, NCBIP:136581)
C;Genetics:
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 212;
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                                45
                                                                4 HGSLTKAGKVRKQTPRLPAKQ--KKNYPPRLKNRLKYQVRIEKV 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: Escherichia coli ribosomal protein L4 C;Keywords: protein biosynthesis; ribosome
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Pred. No. 7.1;
7; Mismatches
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Best Local Similarity 37.0%;
Matches 20; Conservative
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                                                                                                                      A,Accession: S18183
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-229 «RUE>
A;Cross-references: EMBL:X75315
C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotei
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyx A;Reference number: A72450; MUID:99310339; PMID:10382966
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A.Experimental source: strain Kl
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A; Description: Sulfolobus solfataricus complete genome.
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-52 <KUR>
A;Cross-references: GB:AE006641; NID:g13814118; PIDN:AAK41214.1; GSPDB:GN00155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1SU ribosomal protein S30E (rps30E) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: G90244
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R;Ruehlmann, A.; Gupta, A.; Terworst, C.
submitted to the EMBL Data Library, September 1993
A;Description: A movel murine RRM-type protein and its human homolog.
A;Reference number: $38382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1,
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Pred. No. 0.0041;
5; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                        35.2%; Score 107; DB 2; L 100.0%; Pred. No. 0.00034; ive 0; Mismatches 0;
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Best Local Similarity 52.3%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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A;Molecule type: DNA
A;Residues: 1-50 <KAW>
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Best Local Simi
Matches 20;
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Best Local
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nucleocapsid protein - murine hepatitis virus (strain 3)
C;Species: murine hepatitis virus, MHV
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: B45340
R;Parker, M.M.; Masters, P.S.
Virology 179, 463-468, 1990
A;Title: Sequence comparison of the N genes of five strains of the coronavirus mouse hep A;Reference number: A45340; MUID:91021052; PMID:2171216
A;Accession: B45340
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B45340
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C;Superfamily: coronavirus nucleocapsid protein
C;Keywords: glycoprotein; nucleocapsid
F;409,422/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: coronavirus nucleocapsid protein
C;Keywords: glycoprotein; nucleocapsid
F;409,422/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Search completed: December Job time : 22 secs
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A; Residues: 1-454 < PAR>
                                                                                                                                                                                                         Query Match 21.2%; Score 64.5; I Best Local Similarity 36.4%; Pred. No. 19; Matches 20; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.2%; Score 64.5; DB 1; Length 454; Best Local Similarity 36.4%; Pred. No. 19; Matches 20; Conservative 8; Mismatches 24; Indels 3
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                                                                                                 6 LARAGKVRGQTPKVAKQEKK--KKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNAN 58
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 GenCore version 5.1.3 (c) 1993 - 2002 Compugen
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Q96690 oryzias lat
P49689 arabidopsis
O96269 plasmodium
O42952 schizosacch
Q12087 saccharomyc
Q99919 aeropyrum p
P03416 murine coro
P18448 murine coro
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Q12915 rat coronav
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Q02915 rat coronav
P18446 murine coro
Q0470 drosophila
P2658 gallus gall
Q05753 arabidopsis
Q9nq38 homo sapien
P27418 euglena gra
P34396 caenorhabdi
P26583 homo sapien
P1741 sus scrofa
P02895 plasmodium
P47398 mycoplasma
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"The carboxyl protein S30."; J. Biol. Chem. [4] SEQUENCE FROM 1 SPECIES=Mouse; MEDLINE=952415; MARAMURA M., XX "Molecular clor nonspecific supproc. Natl. Acc [5] SEQUENCE FROM 1 SPECIES=Mouse; MEDLINE=952933; Casteels D., P	TAE GENCE	Homo sapiens (Human Homo sapiens (Mouse Rattus norvegicus (Cricerulus griseus Sus scrofa (Pig) Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606, 10 SEQUENCE FROM N.A. SPECIES=Human; WEDLINE=92412144; PREDLINE=92412144; PREDLINE=92412144; Prochem Honbyes Briochem Honbries Briochem Honbries Riochem Honbries Riochem Honbries Respectations Sequencia Respectations Respectatio	N HUMAN 72; Q95 UN-1994 UN-1994 CT-2001	55 56 57 56 57 56 57 56 57 57 57 57 57 57 57 57 57 57 57 57 57
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tin-like protein i ).  u T., Tanigawa Y.; tion of a CDNA enc 63-3467(1995). E=Liver; L., Merregaert J.;	van Hasselt F., K S30 fusion protein in the Finkel-Bisk	), and ata; Vertebrata; E rhini; Hominidae; 9, 9823; 9, 9823; f the human fau ge f the human fau ge f cyr-qan(1992).	ALIGNMENTS  RT; 59 AA.  ence update) tation update)	ACHD ACSU 22 22 24 24 25 26 27 27 27 27 27 27 27 27 27 27 27 27 27
e rat roding m	s K., and i s-Rei	Auteleos Homo.		Q9k8a0 P39120 P36934 O14185 O128409 P45909 P63328 P02286 Q9u1w0 P52362 Q60284
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mouse Fau gene: genomic structure, chromosomal localization, and
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                                                                                                                            1 KVHGSLARAGKVRGQTPKVAKQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KVHGSLARAGKVRGQTPKVAKQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Taleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha, Beloniformes, Adrianichthyidae, Oryziinae, Oryzias.
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                                                                      SPECIES=C.griseus;
Rossman T.G., Wang Z.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 AA; 6648 MW; 012AC1FB555B01A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryzias latipes (Medaka fish) (Japanese ricefish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            090670.
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
FAU OR RPS30.
               characterization of two retropseudogenes.";
Genomics 25:291-294(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, X65921; CAA46714.1; ALT INIT.
EMBL, X65923; CAA46716.1; ALT_INIT.
EMBL, X62671; CAA44546.1; -1
EMBL, X65922; CAA46546.1; ALT_INIT.
EMBL, X65922; CAA46715.1; ALT_INIT.
EMBL, D26610; BAA05655.1; ALT_INIT.
EMBL, L33715; AAA91564.1; ALT_INIT.
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MEDLINE=20070552; PubMed=10603084;
Henrich T., Wittbrodt J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, U72543; AAB52915.1;
PIR, JC1278; JC1278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U41499; AAA83776.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:3597; FAU.
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                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (RPB30B).
SETRAIN=CV. Columbia;
MEDLINE=20083488; PubMed=10617198;
MAYER K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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STRAIN=cv. Columbia;
MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Rapi G., Van Aken S., Umayam L., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
              differentially expressed genes.";
Dev. Genes Evol. 210:28-33(2000).
-!- MISCELLANEOUS: THIS RIBOSOMAL PROTEIN IS SYNTHESIZED AS A
C-TERMINAL EXTENSION PROTEIN (CEP) OF A UBIQUITIN-LIKE PROTEIN.
-!- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KVHGSLARAGKVRGQTPNVDKHEEKEEEDGRAKRRIQYNRRFVNVVVTFGKKKGANANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVHGSLARAGKVRGQTPKVAKQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Sequence and analysis of chromosome 2 of the plant Arabidopsis
  in situ hybridization screen for the rapid isolation of
                                                                                                                                                                                                                                                                                                                                                                            Length 59;
                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regad F., Lescure B.; (OCT-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                   E91B9C088C7772CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                      Score 254; DB 1;
Pred. No. 2.3e-23;
5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #99689; 082203; 09M084;
01-FBB-1996 (Rel. 33, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
40S ribosomal protein 330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RPS30A OR AT2G19750 OR F6F22.22) AND (RPS30B OR AT4G29390 OR F17A13.210) AND (RPS30C OR AT5G56670 OR MIK19.12).
                                                                                                                                                                                                                                                                                         EMBL; AJ238274; CAB40969.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                        83.1%;
                                                                                                                                                                                                                                                                                                                 Ribosomal protein.
SEQUENCE 59 AA; 6660 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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STRAIN=cv. Columbia;
Lebas M., Regad F., Le
Submitted (OCT-1993) t
                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              49;
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RA Van der Schueren J. Grymonprez B., Chuang Y.-J., Vandenbussche F., RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Remped S., Feldpausch M., Lamberth S., Van den Daele H., RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., RA Mooijman P., Klein Lankhorst R., Caselen J., Vilarroel R., De Clercq R., RA Derkova D., Bloecker H., Scharfe M., Grimm M., Lamberth S., Van den Daele H., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., RA Dorkova D., Bloecker H., Scharfe M., Grimm M., Loebnert T.-H., Destert R., Rajandream M.A., Lyne M., Benes V., Rechmann S., Argiriou A., Vitale D., Liguori R., Piravandi E., Heller R., Grimm M., Loebnert T.-H., RA Messenet O., Quigley F., Clabauld G., Muendlein A., Felber R., Schnaidt W., Lecharny A., Aubourg S., Ra Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A., RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A., RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C., RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C., RA Fishman D., Hasse D., Lemcke K., Mewes H.-W., Stocker S., Steele J., Rodrigus M., Bartelle P., Courteny L., Cloud J., Abbott A., Sciocker S., Scheel J., Wan E., Cordes M., Abu-Threideh J., Ra Kramer J., Fulcon L., Mardis E., Dante M., Pepin K., Hillier L., RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., Ra Kramer J., Standt R., Johnson G., Geisel C., Layman D., Ra Minx P., Berghoff A., Jones K., Drone K., Cotton M., Joshu C., RA Autonoiu B., Zidanic M., Strong C., Sun H., Lenars B., Yordan C., Schal R., Martienssen R., Marked A., Lander M., Johnson A., Rodriguez M., Hamer B., Yordan C., Schal R., Martienssen R., Marked A., Lochim M., Johns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Columbia; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by t SSP consortium (Salk/Stanford/PGEC)."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There as a use by non-profit institutions as long by non-profit institutions as long modified and this statement is not removed. Use entities requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural analysis of Arabidopsis thallana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned P1 and TAC clones.";
DNA Res. 5:203-216(1998).
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Kotani H., Nakamura Y., Sato S., Asamizu
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Z26869; CAA81482.1; -. AC005169; AAC62141.2; -. AL161574; CAB79697.1; -. AL096692; -; NOT ANNOTATED AB013392; BAB09885.1; -.
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Bilham L., Robben J.,
Bilham L., Robben J.,
Vandenbussche I
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Schizosaccharomyces pombe (Fission yeast).

Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                         TRS30_SCHPO STANDARD; PRT; 61 AA.
042952; 0014314;
15-DEC-1998 (Rel. 37, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
40S ribosomal protein S30.
(RPS30A OR RPS30 OR SPAC19B12.04) OR (RPS30B OR SPBC19G7.03C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind I Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J., Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G., Claycon R., White O., Smith H Praser C.M., Adams M.D., Venter J.C., Hoffman S.L.; "Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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-i- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
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Eukaryota; Alveolata;
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Pred. No. 1.1e-15;
8; Mismatches 10
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                                                                                                                                                                                                                                                                                                    MEDIANES/18 Mode 11859360;

MEDIANES/18 Mode 11859360;

Mode V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sequoros U., Peat N., Hayles J., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., A Brown D., Brown S., Chillingworth T., Churcher C.M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Hurckle E.J., Hunt S., Jagglo R., A James K., Jones L., Jones M., Leather S., McDonald S., McLean J., R. Monorey P., Moule S., Mungall K., Murphy L., Nibhett D., Odell C., R. Monorey P., Mungall K., Murphy L., Nibhett D., Odell C., R. Rutter S., Saunders D., Seeger K., Sharp S., Stevens K., Stevens K., Stevens K., Stevens K., A Taylor K., O'Neil S., Paragues R., Squares S., Stevens K., Mhitchead S., Modward J., Volckaert G., Aert R., Robben J., Grymonprez B., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Modward J., Volckaert G., Aert R., Robben J., Grymonprez B., Modeler K., Taylor R.G., Holzer E., Mosell D., Muriel B., Reinhardt R., Purnelle B., Berry C., Ender M., Schaefer M., Mulbert S., Acalibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S., Lolaure V., Mottier S., Loras M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G., Jucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G., Jucas M., Rochet M., Gallardin C., Moore K., Hurst S.L., Manguez A., Revuelta J.L., Moremo S., Armstrong J., Porsburg S.L., Armstrong J., Norsen D., Murse P., Marcher M., Marker B., Marcher B., Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: THERE ARE TWO GENES FOR $30 IN S.POMBE.
-!- SIMILARITY: BELONGS TO THE $30E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS
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                                                                                                                               Lenaers G., Perret E., Bonnet C., Caput D., Picard A.; "Transcription of ribosomal genes is down regulated by ammonium starvation in fission yeast." Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosomal protein, Multigene family.
SEQUENCE 61 AA, 6910 MW, 4B9C171F1A326F22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-EGC-1998 (Rel. 37, Last annotation update)
40S ribosomal protein 530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
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                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (RPS30A AND RPS30B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.9%;
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     Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                 SEQUENCE FROM N.A.
                                NCBI_TaxID=4896
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01-NOV-1997 (
01-NOV-1997 (
15-DEC-1998 (
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Q12087;
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RS30_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (RPS30A).
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
Johnston M., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
Johnston L., Langston Y., Larreille P., Le T., Mardis E., Menezes S.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (RPS30B).
Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- MASS SPECTROWHETR; MW=6987; MW ERR=3.4; METHOD=MALDI.
-!- MISCELLANEOUS: THERE ARE TWO GENES FOR $30 IN YEAST.
-!- SIMILARITY: BELONGS TO THE $30E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                           Baker R.T., Williamson N.A., Wettenhall R.E.H.,
"The yeast homolog of mammalian ribosomal protein S30 is expres
from a duplicated gene without a ubiquitin-like protein fusion
sequence. Evolutionary implications.";
J. Biol. Chem. 271:13549-13555(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson R., Waterston R.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 AA; 6987 MW; 65EADAED8D9FC586 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.7%; Score 175.5; DB 1
62.7%; Pred. No. 3.8e-14;
iive 6; Mismatches 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
30S ribosomal protein $30.
ABSJOE OR APSSOG8.
Aeropyrum pernix.
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                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE (RPS30A)
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                                                                                                                                                                                                                 STRAIN=YRB141;
MEDLINE=96278780; PubMed=8662789;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCA1_CVMA5
P03416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVMA5
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                                                                                                                                                                                                                                                                                                                                                                                           Armstrong J., Smeekens S., van der Zeijst B.A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine coronavirus MHV (strain Viruses; ssRNA positive-strand Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel.
01-NOV-1988 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Complete proteome. SEQUENCE 50 AA; 5701 MW; 346A9DABD4E67DCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                   Molecular biology and pathogenesis of coronaviruses, Plenum Press, New York (1984).
                                                                                                                                                                                                                                                                                                                                         coronavirus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Armstrong J., Smeekens S., Rottier P.J.M., "Sequence of the nucleocapsid gene from mu Nucleic Acids Res. 11:883-891(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=83168908; PubMed=6687635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleocapsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP000063; BAA81211.1;
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                                                                                                                                                                                                                                                                              (In) Rottier P.J.M., van der Zeijst B.A.M.,
Horzinek M. (eds.);
                                                                                                                                                                                                                                                                                                                                                               "Cloning and sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=11142;
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(Rel. 09, Last sequence update)
(Rel. 41, Last annotation updat
protein (Version 1).
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                                                                                                                                                                                                                                                                                                                                                                     of the
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Pred. No. 0
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viruses, no DNA stage; Nidovirales;
                                                                                                                                                                                                                                                                                                                                                               nucleocapsid
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                                                                                                                                                                                                                                                                                                       Spaan W.J.M.,
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RESULT
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Best Local S
Matches 20
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                                                       NCA2_
 P18448;
01-NOV-1990
01-NOV-1990
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
-i- PUNCTION: THIS PROTEIN BINDS DIRECTLY AND SPECIFICALLY TO
                                                                                                                                                                                                                                         InterPro; IPR002136; Ribosomal_L4/L1E.
Pfam; PF00573; Ribosomal_L4; 1.
Ribosomal protein; rRNA-Binding; Complete proteome.
SEQUENCE 212 AA; 23589 MW; 58421C03A2754D0B CRC64;
                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
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STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOS ribosomal protein L4. RPLD OR MPN166 OR MP665.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herrmann R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 LAKLGKDAGQPKQVTKQSAKKVRQKILNKPRQKRTPNKQCPVQQCFG-KRGPNQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RRNA (BY SIMILARITY). SIMILARITY: BELONGS TO THE L4P FAMILY OF RIBOSOMAL PROTEINS
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                                                                                                                             SILTKGEVRGG----GKKPYKQKHTGKARQGSTRNPHFVGGGIVFGPK--PNRN
                                                                                                                                                       SLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNAN
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l Similarity 37.0%;
20; Conservative
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38.2%;
Created)
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                                                                                                                                                                                  Score 66; DB 1;
Pred. No. 0.84;
7; Mismatches
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             454
Nucleocapsid
                                         Local S...
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NCAP_CVRSD
ID _NCAP_CVRSD
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                                                                                     SEQUENCE FROM N.A. MEDLINE=91021052; PubMed=2171216; Parker M.M., Masters P.S.; Sequence comparison of the N genes of five strains of the "Sequence comparison of the N genes of five strains of the Coronavirus mouse hepatitis virus suggests a three domain structure for the nucleocapaid protein."; Virology 179:463-468(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91021052; PubMed=2171216;
Parker M.M., Masters P.S.;
"Sequence comparison of the N genes of five strains of the coronavirus mouse hepatitis virus suggests a three domain structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine coronavirus MHV (strain 3).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                          Murine coronavirus MHV (strain A59).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 LAKLGKDAGQPKQVTKQSAKEVRQKILNKPRQKRTPNKQCPVQQCFG-KRGPNQN 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      LARAGKVRGOTPKVAKOEKK--KKKTGRAKRRMOYNRRFVNVVPTFGKKKGPNAN 58
                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                            24; Indels
                                                                                                                                                                                                                                                                                                                                                                          49587 MW; 4992187AB0EB131E CRC64;
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01-NOV-1990 (Rel. 16, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                Score 64.5; DB Fred. No. 2.7; 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 AA
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PIR; C45340; C45340.
InterPro; IPR001218; Corona_nucleocap.
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PIR; B45340; B45340.
InterPro; IPR001218; Corona_nucleocap.
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                                                                                                                                                                                                                                                                                                                                     Pfam; PF00037; Corona_nucleoca; 1.
Nucleocapsid.
SEQUENCE 454 AA: 49587 MM4.
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Nucleocapsid protein (Version 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for the nucleocapsid protein."; Virology 179:463-468(1990).
                                                                                                                                                                                                                                                                                                                                                                                                  21.2%;
                                                     Coronavirus.
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                                                               NCBI_TaxID=11142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11140;
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"Sequence comparison of the N genes of five strains of the coronavirus mouse hepatitis virus suggests a three domain structure for the nucleocapsid protein.";
Virology 179:463-468(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine coronavirus MHV (strain S).
Yitubes; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                          242 LAKLGKDAGQPKQVTKQSAKEVRQKILNKPRQKRTPNKQCPVQQCFG-KRGPNQN 295
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                                                     Score 64.5; DB 1; Length 454; Pred. No. 2.7;
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49687 MW; 9C46DB2317E3A849 CRC64;
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Nucleocapsid protein.
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
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Pfam; PF00937; Corona nucleoca; 1.
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36.4%;
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                                                     21.2%;
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                                                                                                                 Conservative
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01-NOV-1990
01-NOV-1990
01-AUG-1991
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                                                                                                                                                                                                                                                                            Parker M.M., Masters P.S.;
"Sequence comparison of the N genes of five strains of the coronavirus mouse hepatitis virus suggests a three domain structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                           modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                             Murine coronavirus MHV (strain Viruses; ssRNA positive-strand Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00937; Corona_nucleoca; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                           PIR; D45340; D45340.
InterPro; IPR001218; Corona_nucleocap.
                                                                                                                      EMBL; M35253; AAA46439.1;
                                                                                                                                                                                                                                                        for the nucleocapsid protein."; Virology 179:463-468(1990).
                                                                                                                                                                                                                                                                                                                         MEDLINE=91021052; PubMed=2171216;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleocapsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D10760; BAA01591.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virology 193:520-523(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coronavirus SDAV-681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of the
                                                                            Pfam; PF00937; Corona_nucleoca;
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=11139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001218; Corona_nucleocap.
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 Local Similarity
nes 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LARAGKVRGQTPKVAKQEKK--KKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNAN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO NUCLEOCAPSID PROTEINS OF MURINE CORONAVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A45396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
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20; Conservative
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  Conservative
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16, Last sequence up
19, Last annotation
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                                                    49694 MW;
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Score 64.5; DI
Pred. No. 2.7;
8; Mismatches
 8
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Pred. No. 2
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1 viruses,
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time :
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P03417;
21-JUL-1986
                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             "Coronavirus JHM: nucleotide sequence
                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVMJH
                                                                                                                                                                             Nucleocapsid.
                                                                                                                                                                                        Pfam; PF00937; Corona_nucleoca;
                                                                                                                                                                                                                      PIR; A04024; VHIHMJ.
                                                                                                                                                                                                                                   EMBL; X00990; CAA25497.1; -.
                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 11:5045-5054(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine coronavirus MHV (strain
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                                                                                                                                                                                                                                                                                                                                                                                      nucleocapsid protein.
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                                                                                                                                                                                                        InterPro; IPR001218; Corona_nucleocap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 LAKLGKDAGQPKQVTKQSAKEVRQKILNKPRQKRTPNKQCPVQQCFG-KRGPNQN 295
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                                                                                                                        Local
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                                                                                6 LARAGKVRGQTPKVAKQEKK--KKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNAN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LARAGKVRGQTPKVAKQEKK--KKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNAN
                                                      LAKLGKDAGOPKOVTKOSAKEVROKILNKPROKRTPNKOCPVOOCFG-KRGPNON 295
12 secs
                                                                                                            20;
                                                                                                                      Similarity
                                                                                                                                                                 455 AA; 49714 MW; 36FC529D1272B5BE CRC64;
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                                                                                                            Conservative
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                                                                                                                      21.2%;
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            2002,
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Pred. No. 2.7;
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Result
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               104.5
101.5
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87.5
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304
288
269
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231
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     100.0
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304
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sp_bacteria:*
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sp_phage:*
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sp_mammal:*
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  Q962Q1
Q9VDH8
Q9VDE8
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Q97ZH4
Q97ZH4
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Q8ZRO5
Q8ZV51
Q9LG56
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Q91V99
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Q920W8
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Q9h5v4 homo sapien
Q9jj24 mus musculu
Q920w8 mus musculu
Q920w7 mus spicile
Q91v99 mus musculu
Q90yp1 ictalurus p
Q962q1 spodoptera
Q9vdh8 drosophila
Q9wdh8 drosophila
Q9m0e4 arabidopsis
Q18231 caenorhabdi
Q15351 homo sapien
Q972h4 sulfolobus
Q8zv51 pyrobaculum
Q91g56 oryza sativ
                                                                                                                                                                                          Description
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<b>4</b> 5	44	43	42	41	40	9	38	37	36	35	34	33	32	<u>3</u> 1	30	29	28	27	26	25	24	23	22	21	20	19	18	17
60	60	60	60	60.5	60.5	61	61.5	61.5	62	62	62.5	63	63	63	63	63.5	63.5	63.5	63.5	64	64.5	64.5	64.5	64.5	64.5	64.5	64.5	64.5
19.7	19.7		19.	19.	19.	20.	20.	20.																			21.2	
893	521	435	115	731	351	317	836	171	917	467	454	517	421	290	260	1510	451	451	451	225	457	455	455	454	454	454	451	425
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Q8WZS5	042650	Q940Y0	Q64390	060433	Q9CW80	Q9U613	Q9WTY8	Q9LDA1	Q9VBX5	Q8R6I7	Q91KC6	Q9LXR2	Q9BL55	Q99463	Q9LGZ9	Q25920	96Ad6Ö	072588	Q9J3F6	Q8YYX5	Q08614	Q9QCZ9	Q83360	Q9J3E2	Q9WCD0	Q83358	Q83359	Q83357
Q8wzs5 neurospora	O42650 schizosacch	Q940y0 arabidopsis	Q64390 rattus norv		Q9cw80 mus musculu	Q9u6l3 artemia san	rattue	Q9ldal oryza sativ		Q8r6i7 t hypotheti	Q9ikc6 rat sialoda	Q91xr2 arabidopsis	Q9b155 caenorhabdi	Q99463 homo sapien	Q9lgz9 arabidopsis	lasmod	murine	murine	murine he	anabaeı	murine	murine	Q83360 murine hepa	murine	rat co	murine		Q83357 murine hepa

### ALIGNMENTS

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RESULT 1
Q9H5V4
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                                                                                                                                   Query Match
Best Local S
Matches 59
                                                                                                                              InterPro; IPRO002626; Ubiquitin.

Pfam; PF00240; ubiquitin; 1.

PRINTS; PR00348; UBIQUITIN.

SMART; SM00213; UBQ; 1.

PROSITE; PS00299; UBIQUITIN 1; 1.

PROSITE; PS50053; UBIQUITIN 2; 1.

SEQUENCE 133 AA; 14390 MW; 5D2F
                                                                                                                                                                                                                                                                                                                                                                                                                    Q9H5V4 PRELIMINARY; PRT; 133 AA.
Q9H5V4;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FLJ22986 fis, clone KAT11742.
HOmo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                   Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashii Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T. Makamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK026639; BAB15515.1; -.
HSSP; P02248; 1UBI.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
75
                 1 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59
KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 133
                                                              ch 100.0%; Score 304; DB 4; Similarity 100.0%; Pred. No. 4.8e-30; Sp; Conservative 0; Mismatches 0;
                                                                                                                                   5D2F81F2A355B559 CRC64;
                                                                                                                                                                                                                                                                                                                                        Yamazaki M., Tashiro H.,
ibahara T., Tanaka T.,
                                                                                                 Length 133;
                                                               Indels
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                                                               Gaps
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RESULT 2

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Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N., "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of Five Mus musculus subspecies.",
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB039086; BAB68610.1; -.
InterPro; IPR000626; Ubiquitin.
PFam; PF00240; ubiquitin, 1.
PROSITE; PS00299; UBIQUITIN 1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N., "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRQYNRRFVNVVPTFGKKKGPNANS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRPVNVVPTFGKKKGPNANS 137
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                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus spicilegus (Steppe mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KVHGSLARAGKVRGQTPKVAKQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 304; DB 11; Length 137; 100.0%; Pred. No. 5e-30; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB039093; BAB68617.1;
Interpro; ISPRO0626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
PROSITE; PS00299; UBIQUITIN 1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER 1 1 - SEQUENCE 137 AA; 14845 MW; 57099FF4055D8B2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER 1 1 SEQUENCE 137 AA, 14787 MW, 57099FF7065D8828 CRC64;
        Last sequence update)
Last annotation update)
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Last annotation update)
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20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
les 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Fau protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fau protein (Fragment).
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                    STRAIN=BLG2/MSF;
                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ZBN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Q91V99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
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Q91V99
ID Q91V9
AC Q91V9
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                                                                                  01-OcT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Monoclonal non-specific suppressor factor beta (Pinkel-Biskis-Reilly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     June G.-Y., Li Y., Salamonsen L.A., Clements J.A., Findlay J.K., "Identification of monoclonal non-specific suppressor factor beta as one of the genea differentially expressed at implantation sites compared to interimplantation sites in the mouse uterus."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVVTFGKKKGPNANS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59
                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
V.CBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                 murine sarcoma virus (FBR-MuSV) ubiquitously expressed) (fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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InterPro; IPR00626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
PRINTS; PR00348; UBIQUITIN.
SMART; SM0213; UBO; 1.
PROSITE; PS00599; UBIQUITIN. 1; 1.
PROSITE; PS0059; UBIQUITIN. 2; 1.
SROSITE; PS0653; UBIQUITIN. 2; 1.
SEQUENCE 113 AA; 11416 MW; 2087C774A022AB16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 304; DB 11;
100.0%; Pred. No. 4.8e-30;
ive 0; Mismatches 0;
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                                  133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
EMBL; AF147745; AAF80246.1; -.
EMBL; AK008466; BAB25684.1; -.
EMBL; AK002355; BAB22034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 59, Conservative
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                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SWISS OB;
                                                                                                                                                                                                                                    derived).
                                  Q9JJ24
Q9JJ24;
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Matches 56
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L'Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL; AB039084; BAB68608.1; -.
R EMBL; AB039085; BAB68609.1; -.
R EMBL; AB039087; BAB68611.1; -.
R EMBL; AB039088; BAB68612.1; -.
R EMBL; AB039089; BAB68612.1; -.
R EMBL; AB039089; BAB68614.1; -.
R EMBL; AB039090; BAB68614.1; -.
R EMBL; AB039091; BAB68615.1; -.
R EMBL; AB039092; BAB68615.1; -.
R EMBL; AB039092; BAB68615.1; -.
R EMBL; AB039092; BAB68615.1; -.
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Best Local (
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01-DEC-2001
01-MAR-2002
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Q90YP1; Preliminary; PrT;
Q10YP1;
Q1-DEC-2001 (TrEMBLrel. 19, Last seq
Q1-DEC-2001 (TrEMBLrel. 20, Last ann
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Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                      Submitted (JÜL-2001) to the EMBL/GenBank/DDBJ EMBL; AF402841; AAK95215.1; IRN00626; Ubiquitin. Pfam; PF00240; ubiquitin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 ribosomal protein 830. Ictalurus punctatus (Channel catfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=VARIOUS STRAINS;
Liu Y., Kitano T., Koide
"Conspicuous Differences
                                                                                                                                                                                                                                           PROSITE; PS50053; UBIQUITIN_2; 1. Ribosomal protein. SEQUENCE 133 AA; 14504 MW; 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Karsi A., Patterson A., Feng J., Liu Z.J.; "Translational machinery of channel catfish: approach to the analysis of 32 40S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7998;
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KVHGSLARAGKVRGQTÞKVAKQEKKKKKTGRAKRRMQYNRRFVNVVÞTFGKKKGÞNANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00240; ubiquitin; 1.
TE; PS00299; UBIQUITIN 1; UNKNOWN 1.
TE; PS50053; UBIQUITIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
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59; Conservative
                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14787 MW;
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100.0%; P
ative 0;
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>ng Gene Gen
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Pred.
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Pred. No. 5e-30;
0; Mismatches
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                                                                                                                                                                                                                                           62036BB0E72C5CAC
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                                                                                                         Mismatches
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No. 4.
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Genealogies of 21 Nuclear Genes
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Ostariophysi; Siluriformes;
                                                                                                                                     DB 13;
.6e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
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MEDLINE=20196006; PubMed=10731132;

XX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

A Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

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A Sutton G.G., Wortman J.R., And H.-J., Andrews-Pfennkoch C., Baldwin D.,

A Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

A Baril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Banso P.V., Berman B.P., Bhandari D., Bolhakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

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A Burtis K.C., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

A Harris N.L., Harryey D., Heiman T.J., Wei M.-H., Ibegwam C.,

Jana Harris N.L., Harryey D., Heiman T.J., Wei M.-H., Ibegwam C.,

Jana Harris N.L., Harryey D., Heiman T.J., Wei M.-H., Ibegwam C.,

Jana Halli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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Matches 50
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Q962Q1;
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Spodoptera frugiperda (Fall armyworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; He
Eukaryota; Neoptera; Endopterygota; Diptera;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9VDH8
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a; Brachycera; Musc
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Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Langko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Li X., Martei B.E., McIncosh T.C., McLeod M.P., McDherson D., Andreis B., McIncosh T.C., Morrow M.P., Moshrefi A., Merkulov G., Milshina N.V., Muscher D.B., Monnt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nalson D.E., Nalson D.E., Nalson D.E., Pacled J. P., Pacled J. P., Pacled J.M., Nan B.C., Scheeler F., Shen H., Shine B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Weilliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., A. J., Yeh R.-P., Zaveri J.S., Zhan M., Zhong Y., Zhu S., Zhong W., Zhou S., Zho S., Zhong W., Zhou S., Zho S., Kollobs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyra, Embryophyra, Tracheophyta,
Spermatophyra, Magnoliophyra, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 KVHGSLARAGKVKGQTPKVEKQEKKKKKTGRAKRRIQYNRRFVNFVQGFGRRRGPNANS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KVHGSLARAGKVRGOTPKVAKOEKKKKKTGRAKRRMOYNRRFVNVVPTFGKKKGPNANS 59
                                                                                                                                                                                                                                                                                                                    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
11-OCT-2000 (TrEMBLrel. 20, Last annotation update)
Ribosomal protein S30 homolog (40S ribosomal protein S30 homolog)
(At2g19750/F6F22.22).
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Lennard N., Quall M., Harris B., Rajandream M.A., Barrell B.G.,
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 132;
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Pred. No. 5.7e-25;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-98403884; PubMed-9734815;
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE003732; AAF55815.1; -.
EMBL, AX071683; AAL49305.1; -.
FlyBase; FBGN0038834; CG15697.
InterPro, IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
SEQUENCE 132 AA, 14585 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n 86.5%;
Similarity 84.7%;
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SEQUENCE FROM N.A.

Kim C.J. Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,

Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,

Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,

Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,

Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,

Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
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                                                                                                                                                                                                                           Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Babn J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Nartuaaka M., Onderera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A. Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Arabidopsis CDNA clones.", Theologis A., Ecker J.R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNAN
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"Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned Pl and TAC clones."; DNA Res. 5:203-216(1998).
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Pred. No. 2.4e-21;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ecker J.R.;
"Arabidopsis ORF clones.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL161574; CAB79697.1;
EMBL; AB013392; BAB09885.1;
EMBL; AY052341; AAK96533.1;
EMBL; AY061910; AAL31237.1;
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Last annotation update)
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1 Similarity 75.9%;
44; Conservative
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SEQUENCE 62 AA;
                                                                                                                                                                                         SEQUENCE FROM N.A.
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RESULT 11
Q15351
  RESULT 12
Q97ZH4
ID Q97ZH
AC Q97ZH
DT 01-OC
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Matches 21
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Best Local Similarity
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Q15351;
01-NOV-1996 (TrEMBLrel. (
01-NOV-1996 (TrEMBLrel. (
01-JUN-2002 (TrEMBLrel. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A novel murine RRM-type protein and its human homolog."; Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases. EMBL; X75315; CAA53064.1; -. HSSP; P09651; IUP1. InterPro. Traccord.
Q97ZH4
Q97ZH4;
Q1-OCT-2001
01-OCT-2001
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Pfam; PF00240; ubiquitin; 1.
SMART; SM00213; UBQ; 1.
SEOUENCE 130 AA; 14033 MW;
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Homo sapiens (Human).
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"The sequence of C. elegans cosmid C26Fl.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Nature 368:32-38(1994).
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Mammalia; Eutheria;
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STRAIN-BRISTOL N2;
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STRAIN=BRISTOL N2;
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PROSITE; PS00030; RRM RNP_1; UNKNOWN_1.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000504; RNA_rec_mot
                                                                                                                                                                                 72 KVHGSLARAGKVRAQTPKVDKQDKKKKKKRGRAFRRVQYTRRYVNVASGPGKKRGPNSNS 130
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                                                                                                                                                                                                                                                                                                Similarity
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  (TrEMBLrel. 18, (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                           Conservative
                                                                       PRELIMINARY;
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Primates;
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76.3%;
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Pred. No. 1.6e
5; Mismatches
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  sequence update)
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                                                                                                                                                                                                                                                                                                                        DB 4;
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RESULT 13
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RC STRAIN=ATCC 35092 / DSM 1617 / P2;

RX MEDLINE=21332296; PubMed=11427726;

RX MEDLINE=21332296; PubMed=11427726;

RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

RA Nayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

RA Charlebois R. J., Doglittle R. F., Daguet M., Gaasterland T.,

RA Charlebois R. L., Doolittle W. F., Duguet M., Gaasterland T.,

RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

RT Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

DR EMBL; AED06714; AAK41214.1;

DR EMBL; AED06714; AAK41214.1;

RSQ SEQUENCE 52 AA; 6046 MW; A9EB9D3E4E7E744E CRC64;
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Best Local S
Matches 21
                                                                                                            Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                              Ribosomal
SEQUENCE
                                                                                                                                                                                                                                                                           PubMed=11572479;

Rawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Kawarabayasi Y., Hino Y., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Yoshizawa T., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

Oshima T., Kikuchi H.;

Oshima T., Kikuchi H.;

Complete genome sequence of an aerobic thermoacidophilic

Crenarchaeon, Sulfolobus tokodaii strain?.";

DNA Res. 8:123-140(2001).

EMBL, AP000985; BAB66306.1;

DNA Res. Bab66306.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q971W4
Q971W4;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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LSU ribosomal protein S30E
RPS30E OR SSO6817.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=JCM 10545 / 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=111955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sulfolobus tokodaii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 51.;
nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 HGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFV 43
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HGSLTKAGKVRNATPKMPKKE-RHKEVPRVRNRIEYEKRVV
                                                                                                                                             Similarity
                                                                                                                                                                                                                              protein; Hypothetical protein; Complete proteome
55 AA; 6365 MW; 5C9404787BA65826 CRC64;
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.4%;
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                                                                                                               Score 101.5; DB 1
Pred. No. 2.3e-05;
9; Mismatches 11
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Pred. No. 9.2e-06;
7; Mismatches 12
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                                                                                                                                                                     DB 17; Length 55;
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Search completed: December 3, 2002, 14:32:53
Job time: 32 secs
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                                                                                                                                                                                                                                                                                      STRAINGE-MI;
MEDLINE-21576510; PubMed=11719806;
Ratinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
Rrainka M.D., Duprat S., Cornillot E., Brottier P., Wincker P.,
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
Weissenbach J., Vivares C.P.;
Weissenbach J., Vivares C.P.;
Weissenbach J., Vivares C.P.;
Weissenbach J., Sequence and gene compaction of the eukaryote parasite
Encephalitozoon cuniculi.";
Nature 414:450-455(2001).
EMBL; AL590449; CAD25878.1;
EMBL; AL590449; CAD25878.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I., Miller J.H.,
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28.8%; Score 87.5; DB 17; Length 55;
Best Local Similarity 48.7%; Pred. No. 0.0012;
Matches 19; Conservative 5; Mismatches 14; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.2%; Score 95; DB 5; Length 59; 45.9%; Pred. No. 0.00016; iive 11; Mismatches 9; Indels
                                                                                                                          Encephalitozoon cuniculi.
Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
NCEL_TaxID=6035;
                                                                                                                                                                                                                            Genoscope; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrobaculum aerophilum.
Archaea, Crenarchaeota, Thermoprotei, Thermoproteales;
Thermoproteaceae, Pyrobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL, AE009977; AAL64205.1; -.
Complete proteome.
SEQUENCE 55 AA; 6200 MW; E2F91102FE9FFF90 CRC64;
                                        01-UUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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             59 AA
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STRAIN=IM2 / ATCC 51768 / DSM 7523;
PubMed=11792869;
             PRT;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 45.9%
Matches 17; Conservative
                                                                                           40S ribosomal protein S30.
             PRELIMINARY;
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                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=GB-M1;
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           Q8SR05
Q8SR05;
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Q8SR05
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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    2022222111111111
20222221111111111
20542220987654
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54.5
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304
1 KVHGSLARAGKVRGQTPKVA.....RRFVNVVPTFGKKKGPNANS
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123.997 Million cell updates/sec
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    Copyright
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US-08-415-818-12
US-08-894-236-12
PCT-US96-0.144-12
US-09-615-192A-378
US-09-615-192A-378
US-09-9134-001C-5286
US-09-924-864-36
US-09-924-333-3
US-09-615-192A-389
US-09-615-192A-389
US-09-615-192A-389
US-09-134-001C-330-5
US-09-245-041-11
US-09-245-041-11
US-09-245-041-11
US-09-245-041-11
US-09-245-041-11
US-09-245-041-11
US-09-245-041-11
US-09-245-041-11
US-09-245-041-11
US-09-345-041-11
US-09-345-041-11
US-08-346-277
US-08-39-39-819-11
US-08-39-39-819-2
US-08-384-212-1
US-08-384-213-1
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Compugen Ltd.
       Sequence 8, Appli
Sequence 57, Appl
Patent No. 5310667
Sequence 119, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
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Patent No.
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12, Appl
12, Appl
378, App
5286, Ap
5286, Ap
1, Appli
1, Appli
3, Appli
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3, Appli
3305, Ap
11, Appl
57, Appl
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 Query Match
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45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28
•	51.5	•			•		•	•		•		•	•	52	52	52	52
16.9								16.9							17.1	17.1	17.1
1863	1852	1852	1363	1363	1202	1202	801	472	472	59	59	59	59	154	154	143	139
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US-08-425-061-16	US-08-825-886-24	US-08-425-061-24	US-08-825-886-23	US-08-425-061-23	0	US-08-425-061-22	US-09-104-070-2	US-09-115-746-10	US-08-216-894-10	US-08-462-040-60	-08-460-971A	US-08-167-641C-60	US-08-460-890A-60	US-09-346-510B-1	US-08-871-732A-1	US-08-464-841A-4	US-08-464-841A-2
Sequence 16,	Sequence 24,		Sequence 23,		Sequence 22,	Seguence 22,	Seguence 2,	Sequence 10,	Sequence 10,	Sequence 60,		Seguence 60,		Sequence 1,	Sequence 1,	Sequence 4,	Sequence 2,
, Appl	, Appl	•	, Appl	•	-	, Appl	Appli	, Appl	•	•	•	•		Appli	Appli	Appli	Appli

### ALIGNMENTS

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RESULT 1
US-08-415-818-12
US-08-415-818-12
                                                                                  APPLICATION NUMBER: US/08/415
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/383,74
FILING DATE: 03-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: APPOLITINA, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 1939
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3462
TELEFAX: 908-594-3462
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acids
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
               STRANDEDNESS: 811
TOPOLOGY: linear
MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Mary A. Appollina STREET: P.O. Box 2000, 126 E. Lincoln CITY: Rahway STATE: NJ COUNTRY: USA ZIP: 07065
                                                                        amino acid
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Tan, Carina P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shiao, Lin-Lin
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Linemeyer, David L.
                 protein
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20.7%;

Score

63;

DB 1;

Length 370;

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STREET: P.O. CITY: Rahway
                                                                                                                                                                                                                                                                                         USA
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                     Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NN-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,236
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                       13;
                                                                                                                                                                                                                                                         APPLICANT: CASCIETI, MATGATET A.
APPLICANT: Linemeyer, David L.
APPLICANT: MacNeil, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
Best Local Similarity 38.7%; Pred. No. 1.7;
Matches 12; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                       241 AKVDKKKENEGRLNENKRINTMLISIVVTFG 271
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                                                           20 AKQEKKKKKTGRAKRRMOYNRRFVNVVPTFG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 AKQEKKKKKTGRAKRRMOYNRRFVNVVPTFG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,746
FILING DATE: 03-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/415,818
FILING DATE: 03-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application PC/TUS9601444 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19390Y
                                                                                                                                                                                                   Sequence 12, Application US/08894236
Patent No. 5939263
GENERAL INFORMATION
APPLICANT: Cascieri, Margaret A. APPLICANT: Linemeyer, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INTERNATION

MAME: Appollina, Mary A.

REGISTRATION NUMBER: 34,087

REFERENCE/DOCKET NUMBER: 1939G

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-594-3462

INFORMATION FOR ESO ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 370 anino acids

TYPE: amino acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 38.7
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NJ
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
PCT-US96-01444-12
                                                                                                                                                                                  US-08-894-236-12
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APPLICANT: Casciert, Margare A.
APPLICANT: Linemayer, David L.
APPLICANT: Machine David L.
APPLICANT: Machine David L.
APPLICANT: Machine David L.
APPLICANT: Shado, LintLin D.
APPLICANT: Wathber David H.
APPLICANT: Nalway A. APPLICANT David H.
APPLICANT: Nalway David H.
APPLICANTION DAVE DAVID H.
APPLICANTION NAMES: Percent T. Release H.O. Version H.1.30
COMPTRIS: Break P. Co-Compatible
COMPTRIS: Break P. Compatible
COMPTR
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PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5286
LENGTH: 171
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-134-001C-5286
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; SOFTWARE: FASTSEQ
; SEQ ID NO 378
; LENGTH: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: LYNT DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                       Sequence 1, Application US/08903801 Patent No. 5932712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Eucalyptus
                                                                                                                                         APPLICANT: Hillman, Jennif
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
                                                                                       APPLICANT: Shah Purvi
TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        166 TSQRGG 171
                                                                                                                                                                                                                                                                                                                                                                                                             106 LVQAGKSLKRLQKQLERARYEVRGQSDEYERMKKRKLAQNKRNREAQKQGTRRFMNSLRN 165
                                                                                                                                                                                                                                                                                                                                                                         49 FGKKKG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 APNNNS 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 SIVRAG-----VAKAIKNETRTGASLLRLHFHDCFVNGCDASILLDDTPSFVGEKTA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 21; Conserv
                                                    STREET:
COUNTRY:
                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LARAGK------VRGQTPKVAKQEKKKKTGRAKR--RMQYNRRFVNVVPT 48
                                                                                                                                                                                                     INFORMATION:
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                                                  3174 Porter Drive
 USA
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                                                                     Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1998-10-09
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                                                                                                                                                                                Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.9%; Score 54.5;
25.8%; Pred. No. 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09295055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: PROSN
CLONE: 2272281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
LENGTH: 290 amino acio
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 ASEEKAETPTAAEDDNEGDKKKKDKKKKKGEKEEKEKE-----
                                                                                                                                                                                                                                                                                                            STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: STRANDEDNESS: 8444
                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: Herewi
                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AGKVRGQTPKVA------KQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94304
                                                                                                                                                                                                                                                                                                                                                E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillman, Jennif
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSNON01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.8%; Score 54; DB 2; Length 290; 26.3%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jennifer
                                                                       08/903,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/903,801
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/241,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Sequence 36, Application US/09724864

Sequence 36, Application US/09724864

Setent No. 6380362

GENERAL INFORMATION:
APPLICANT: Warson, James D.
APPLICANT: Warson, James G.
TITLE OF INVENTION: Polynucleotides and methods for their use.
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.1050U1

CURRENT FILING DATE: 2000-11-28

FRIOR PELICATION NUMBER: U.S. No. 6380362 60/171,678

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 36

LENGTH: 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 9 AGKVRGQTPKVA------KQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPN 56
                                                                                                                                                                                                                                                                                                                                                     22;
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Pred. No. 55;
3; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                          Score 54; DB 4; Length 290;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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APPLICANT: Bandman, Olga
APPLICANT: Vue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN NUCLEOLIN-LIKE PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                        17.8%; Score 54; 22.26.3%; Pred. No. 19; tive 10; Mismatches
PF-0354 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08990114
Parent No. 5932475
GENERAL INFORMATION:
                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.8%;
30.6%;
                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 290 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE:
  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.3%
Matches 15; Conservative
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Best Local Similarity 30.6
Matches 15; Conservative
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                                                                                                                                                                                                                                LIBRARY: PROSNON01
CLONE: 2272281
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Rat
US-09-724-864-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -09-724-864-36
                                                                                                                                                                                                                                                                        US-09-295-055-1
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                                                                                TELEX:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09241333
Patent No. 631326
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Vue, Henry
APPLICANT: Corley, Nail C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HIWAN NUCLEOLIN-LIKE PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Parter Drive
CETTY: Palo Alto
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OFFRATING SYSTEM: DOS
SOFTWARE: FRANCHELLE
OPERATING SYSTEM: DOS
SOFTWARE: FRANCHELL
APPLICATION DATA:
APPLICATION NUMBER: US/08/990,114
FILLING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/990,114
FILLING DATE:
APPLICATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 560-855-0555
TELEPHONE: 650-855-0555
TELESPAN: DOCKET NUMBER: TELESPAN: DOCKET NUMBER: TELESPHONE: 650-855-0555
TELESPAN: DOCKET NUMBER: TELESPAN: DOCKET NUMBER: TELESPHONE: 650-855-0555
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23.7%; Pred. No. 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 714 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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CLONE: 128842
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Best Local Similarity
Matches 18; Conserv
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ATTORNEY/AGENT INFORMATION:

DATE:

APPLICATION NUMBER: 08/990,114

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US-09-615-192A-389
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                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 11000.1003c4U

CURRENT APPLICATION NUMBER: US/09/615,192A

CURRENT FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 08/975,316

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: US 08/713,000

PRIOR FILING DATE: 1996-09-11

PRIOR FILING DATE: 1996-09-11

PRIOR PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                   US-09-615-192A-389
                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 389
LENGTH: 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 389, Application US/09615192A Patent No. 6410718 GENERAL INFORMATION:
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                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
                                                                                                                                                                                                                 ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0451 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: GenBaction 128842
82
                               44
                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 VVSQTKKVAVPTPAKK 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 714 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATFTGEKTAGPNANS 97
                                NVVPTFGKKKGPNANS 59
                                                                                               VHGSLARA--GKVRGQTPKVAKQ-----EKKKKKTGRAKRRMQYNRRFV------ 43
                                                                VNGQLSSTFYAKSCPRLPSIVKSVVKQAVAKEKRMGASLVRLHFHDCFVNGCDGSILLDD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAKAGKTHGEAKKMAPPPKEVEEDSEDEEMSEEEDDSSGEEVVIPQKKGKKATATPAKKV 63
                                                                                                                                 21;
                                                                                                                                                                                                                                                                                   FastSEQ for Windows Version 3.0
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                                                                                                                                 Conservative
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                                                                                                                                               17.4%; Score 53; DB 27.6%; Pred. No. 29;
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23.7%;
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                                                                                                                                                               DB 4; Length 318;
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Lignin Content
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                                                                                                                                 27;
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RESULT 12
US-07-920-281C-3
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                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08466277
Patent No. 6190666
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS.
LENGTH: 1253 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0: FILING DATE: 13-AUG-1992 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DNA ExpressiviTITLE OF INVENTION: Alphaviruses NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Garoff, Henrik APPLICANT: Liljestrom, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Birch, Sto
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 GKVRGQTPKVAKQEKKKKTGRAKR 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             86 GKTQQQKKKDKQADKKKKKPGKRER 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                 ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, St.
STREET: P.O. Box 747
                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                          TITLE OF INVENTION: DNA Expression Systems Based
                                                                                                                                                                                                                                                                          APPLICANT: Garoff, Henrik
Liljestrom, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22040-0747
                                                                                                         STREET: P.O. Box 74
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
GY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1253 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Expression Systems Based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/07/920,281C
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Pred. No. 1.
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20 KKKKKKKKKKKKKKKKKKKKKKKKGRRGAGVRGVYFAGRRLSP 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
17.3%; Score 52.5; D
Best Local Similarity 29.2%; Pred. No. 37;
Matches 14; Conservative 11; Mismatches
                      CURRENT APPLICATION NUMBER: US/09/245,041
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/093,630
EEARLIER FILING DATE: 1998-07-21
EARLIER FILING DATE: 1998-07-21
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 131
SEQ ID NO 11
LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                       LOCATION: all Xaa positions
CTHER INFORMATION: Xaa=unknown amino acid
US-09-245-041-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: December 3, 2002, 14:33:14
Job time : 16 secs
                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                            FEATURE:
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Batent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: BUIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BUIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER FO SEQ ID NOS: 5674

SEQ ID NO 3305

LENGTH: 135
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Sequence 11, Application US/09245041

Patent No. 6274339

GENERAL INFORMATION:
APPLICANT: Moore, K.
APPLICANT: Magle, D.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.4%; Score 53; DB 4; Length 1253; 44.0%; Pred. No. 1.3e+02; tive 5; Mismatches 9; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 GSLKRAGLLT-RDPRM--KERKKPGLKKARRSPQFSKR 135
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,277
FILING DATE: 06-Jun-1995
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY/ACENT INFORMATION:
NAME: MUTPHY Jr. Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-103P
TELECOMMUNICATION:
TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: procein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-466-277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 GKVRGQTPKVAKQEKKKKKTGRAKR 34
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1253 amino acids
                                                                                                                                                                                                                                                                                                                                              TELEX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 44.0
Matches 11; Conservative
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US-09-134-001C-3305
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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seq length: 2000000000
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| ( 'ggn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| ( 'ggn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| ( 'ggn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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                                                  US-09-925-301-994
US-09-864-761-35333
US-09-214-881A-7
US-09-214-881A-7
US-09-864-761-33832
US-09-764-866-7622
US-09-764-866-761-36199
US-09-214-881A-2
US-09-214-881A-2
US-09-214-881A-6
US-09-214-881A-6
US-09-214-881A-6
US-09-764-846-193
US-09-864-761-39624
US-09-864-761-39624
US-09-764-846-229
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Sequence 9, Appli
Sequence 7, Appli
Sequence 33832, A
Sequence 33832, A
Sequence 133, App
Sequence 6139, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 193, App
Sequence 193, App
Sequence 229, App
Sequence 229, App
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
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17.3		17.3	17.3			7.	17.6	7.	17.6	17.6	17.6		7.	17.6	17.8	17.8	17.8	17.8		-	.7	17.9	7.	17.9	17.9
427	427	351	45	1253	63	57	714	498	369	130	130	83	61	58	525	290	141	76	71	150	86	76	76	72	63
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US-09-861-696-57	464-0	-238-	-846-	-901-106-	US-09-764-846-260	US-09-864-761-41286	US-09-978-242-3	-864-	US-09-925-300-1070	US-09-815-242-13732	-242-1201	US-09-864-761-34889	-764-846-1	US-09-764-846-261	US-09-814-550-2	US-09-808-885-1	US-09-864-761-36181	US-10-002-344A-229	US-09-864-761-37061	۲,	US-09-864-761-46660	US-09-764-846-257	_	٠.	US-09-764-846-185
e 57	57,	11,	258	3, Ap	Sequence 260, App	41		e 1122,		13732,	e 12016,	34889	18	261,	2	Sequence 1, Appli	e 361	Sequence 229, App	37061		e 46660	25	e 960,	35548	Sequence 185, App

### ALIGNMENTS

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PRIOR APPLICATION NUMBER: PCT/USO0/05882
PRIOR FILING DATE: 2001-03-08
PRIOR PLICATION NUMBER: PCT/USO0/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 994
RESULT 2
US-09-864-761-35333
US-09-864-761-35333, Application US/09864761
; Sequence 35333, Application US/09864761
; Patent NO. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-994
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REMERAL INFORMATION:

ARPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-09-925-301-994
                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 59; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 170
                                                                                                                                                                                                                                112 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 170
                                                                                                                                                                                                                                                            1 KVHGSLARAGKVRGQTÞKVÁKQEKKKKKTGRÁKRRMQYNRRFVNVVÞTFGKKKGÞNANS 59
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Pred. No. 3.6e-29;
D; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383 01.04
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER: PATENTING DATE: 2999-06-07
SEQ ID NO 9: 13
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 9
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APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 063383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
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US-09-214-881A-7
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LOCATION: (39)
OTHER INFORMATION: Xaa = Glu or Arg
                                                                                                                                                                                                                                                             Sequence 9, Application US/09214881A Patent No. US20020009749A1
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Patent No. US20020009749A1
                                                                                                                                                                                                                                                                                                                                                                  Ozaki, Shoichi
Sobajima, Junko
Usugi, Hiroko
Okazaki, Takahiro
Tanaka, Masao
Nakao, Kazuwa
Yoshida, Michiteru
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Vesugi, Hiroko
Okazaki, Takahiro
Tanaka, Masao
Nakao, Kazuwa
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SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
, ORGANISM: Gallus gallus
US-09-214-881A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD_RES
                                                                      116 ANS 118
57 ANS 59
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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           A PAPLICANT: Handle Land K.

A PAPLICANT: Handle Land K.

A PAPLICANT: Handle Land K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FOR LAND THING DETE: Aconica-x. 12 (9) 464,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PAPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-10-4

PRIOR FILING DATE: 2000-09-27

PRIOR PAPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR PAPLICATION NUMBER: PCT/US01/0066

PRIOR FILING DATE: 2001-01-30

PRIOR PAPLICATION NUMBER: PCT/US01/0066

PRIOR PAPLICATION NUMBER: PCT/US01/0066

PRIOR PLING DATE: 2001-01-30

PRIOR PAPLICATION NUMBER: PCT/US01/0066

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PRIOR PLING DATE: 2001-01-30

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PRIOR PAPLICATION NUMBER: PCT/US01/0066

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PRIOR PRIOR PLING DATE: 2001-01-30

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NY: EXPRESSED IN LUNG, SIGNAL = 19
NY: EXPRESSED IN LUNG, LIVER, SIGNAL = 8.8
NY: EXPRESSED IN PACENTA, SIGNAL = 18
NY: EXPRESSED IN BRAIN, SIGNAL = 5.5
NY: EXPRESSED IN BEAL BARROW, SIGNAL = 9.3
NY: EXPRESSED IN FETAL LIVER, SIGNAL = 4.1
NY: EXPRESSED IN HEAT, SIGNAL = 18
NY: EXPRESSED IN HEAT, SIGNAL = 10
NY: EXPRESSED IN HEAT, SIGNAL = 10
NY: EXPRESSED IN HEAT, SIGNAL = 10
NY: EXPRESSED IN HELA, SIGNAL = 10
NY: EXPRESSED IN HELA
NY: EXPRESSED 
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Pred. No. 4.9e-26;
1; Mismatches 2; Indels
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SOFTWARE: Annomax Sequence Listing Engine vers, 1.1
SEQ ID NO 35333
LENGTH: 118
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Best Local Similarity 88.9
Matches 56; Conservative
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OTHER INFORMATION: EXPRE.
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ORGANISM: Homo sapiens
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INFORMATION: 5
INFORMATION: 6
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US-09-864-761-35333
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                         SOFTWARE: Annomax SEQ ID NO 33832
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Best Local :
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-864-761-33832
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                      TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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OTHER INFORMATION: MAP TO AC007857.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.8
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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Hanzel, David K.
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                                                                                                                                                                           Sequence Listing Engine
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US-09-764-869-722
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                                                                                                                                                                                                      US-09-764-846-163
Prior application data removed -
NUMBER OF SEQ ID NOS: 348
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 163
LENGTH: 66
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prior application data removed - refer to PALM
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 722
                                                                                                                                                            GENERAL INFORMATION:
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                          Sequence 163, Application US/09764846 Patent No. US20020102638A1
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                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteir
FILE REFERENCE: PTZ12
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (56)
OTHER INFORMATION: X
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ORGANISM: Homo :
FEATURE:
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC007
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OTHER INFORMATION:
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Local Similarity 38.2%;
nes 13; Conservative
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34.9%;
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Pred. No. 1;
8; Mismatches
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N HEART, SIGNAL = 6.8
N PLACENTA, SIGNAL = 6.5
N BT474, SIGNAL = 6.5
N BONE MARROW, SIGNAL = 0.1
N FETAL LIVER, SIGNAL = 6.5
N LUNG, SIGNAL = 9.1
N HELA, SIGNAL = 9.1
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ORGANISM: Homo sapiens

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Shirakawa, Hitoshi
Osakada, Fumio
VENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
NCE: 068383.0104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osakada, Fumio
VENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
NCE: 068383.0104
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                                                                                                                                                                                                                                                                                                                                                       19.1%; Score 58; DB 10; Length 72;
41.5%; Pred. No. 1.5;
tive 6; Mismatches 12; Indels
                                                                                                         EXPRESSED IN HELLOO, SIGNAL = 3.5
EXPRESSED IN HEART, SIGNAL = 4.2
EXPRESSED IN BT474, SIGNAL = 2.6
EXPRESSED IN BRAIN, SIGNAL = 3.6
EXPRESSED IN PLACENTA, SIGNAL = 3.8
EXPRESSED IN ADULT LIVER, SIGNAL = 3.8
EXPRESSED IN FILL LIVER, SIGNAL = 3.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 GKRKRKGKRR---RKVRRKKEKKTTRGRGRGRRRRRRR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GSLARAGKVRGQTPKVAKQEKKKKKT---GRAKRRMQYNRR 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/214,881A CURRENT FILING DATE: 1999-06-07 NUMBER OF SEQ ID NOS: 13 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09214881A
Patent No. US20020009749A1
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Patent No. US20020009749A1
OTHER INFORMATION: MAP TO ACOIOG
OTHER INFORMATION: EXPRESSED IN
US-09-864-761-36199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ozaki, Snorca
Sobajima, Junko
Bosugi, Hiroko
F. Okazaki, Takahiro
T. Tanaka, Masao
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Uesugi, Hiroko
Okazaki, Takahiro
Tanaka, Masao
Nakao, Kazuwa
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Shirakawa, Hitoshi
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 41.5'
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
FILE REFERENCE: 060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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TITLE OF INVENTION:
FILE REFERENCE: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tanaka
APPLICANT: Nakao,
APPLICANT: Yoshid
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LENGTH: 208
TYPE: PRT
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US-09-214-881A-6
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US-09-214-881A-2
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APPLICANT:
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APPLICANT: Rank, David R.
APPLICANT: Hancel, David R.
APPLICANT: Hancel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                   DOCATION: (56)
CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-846-163
     LOCATION: (4)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                8
                                                                                                                                                                                         19.4%; Score 59; DB 10; Length 66; 34.9%; Pred. No. 1; tive 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                     1 KVHGSLARAG-----KVRGQTPKVAKQEKKKKKTGRAKRR 35
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-08-30
PRIOR PELING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36199, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                            Query Match
Best Local Similarity 34.9
Matches 15; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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US-09-764-846-193; Sequence 193; Application; Patent No. US20020102638A1; GENERAL INFORMATION:
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US-09-214-881A-8
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; LENGTH: 209
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-214-881A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 8
LENGTH: 209
TYPE: PRT
ORGANISM: Rattus rattus
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CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/764,846 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
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                                                                                                      Prior application data removed - NUMBER OF SEQ ID NOS: 348
                                                         SOFTWARE: PatentIn Ver. 2.0 EQ ID NO 193 LENGTH: 79
                                           LENGTH: 79
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              ORGANISM: Homo sapiens FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                  19 VAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKG----PNA
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5. US20020009749A1
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Nakao, Kazuwa
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                                                                                                                                                                                                                                          Application US/09764846
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Pred. No. 4.6;
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Pred. No.
                                                                                                                    consult PALM
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 209;
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; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-846-193
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                                                                                                                                                           SOFTWARE: Annomax Sequence Listing Engine SEQ ID NO 39624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39624, Application US/09864761 Patent No. US20020048763A1
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Best Local (
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PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR NOTE: 2000-02-04
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CURRENT FILING DATE: 2001-05-22
PRIOR ADDITOR 2001-05-22
                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                      ENGTH: 170
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Local Similarity 34.2%;
les 13; Conservation
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                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00667
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Hanzel, David K.
Chen, Wensheng
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MAP TO AC003664.1
EXPRESSED IN PLACENTA, SIGNAL
EXPRESSED IN LUNG, SIGNAL = 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          001-01-30
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Pred. No.
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Gaps
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                                                                                                         Query Match
Best Local Similarity 30.6%; Pred. No. 1.6;
Matches 15; Conservative 8; Mismatches 13; Indels 1:
                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT212
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 348
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KVHGSLARAGKVRGOTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKK
 MAP TO AC026428.1

EXPRESED IN BONE MARROW, SIGNAL = 0.46

EXPRESSED IN BRAIN, SIGNAL = 0.46

EXPRESSED IN PLACENTA, SIGNAL = 0.49

EXPRESSED IN FETAL LIVER, SIGNAL = 0.46
                                                                                                                                                                      11 KVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59
                                                                                                                                                                                                  -----KKKKQNHHS 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.3%; Score 55.5; D 28.3%; Pred. No. 4; iive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            completed: December 3, 2002, 14:33:30
ne : 12 secs
                                                                                                                                                                                        3 KIKMKTKKTKKRKKKKKKKKKKKK-----
                                                                                                                                                                                                                                                                       ; Sequence 229, Application US/09764846; Patent No. US20020102638A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 28.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-846-229
                               OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-09-864-761-45531
                                                                                                                                                                                                                                              RESULT 15
US-09-764-846-229
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 229
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Θ
                                                                                                            DB 10; Length 170;
CTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
CTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
COTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
US-09-864-761-39624
                                                                                                                                        15; Indels
                                                                                                                                                                      10 GKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKG 54
                                                                                                                                                                                                  ..----GKGKG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/774,203
RICH FILING DATE: 2001-01-29
NUMBER OF SEQ 10 NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                          Score 57; DB pred. No. 4.9; 6; Mismatches
                                                                                                                                                                                        1 : | | : | | | : | | | 25 GKKEKEKEKEKKKKEKEKEKEVENR-
                                                                                                         uvery Match
Best Local Similarity 35.6%;
Matches 16; Conservative 6
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ORGANISM: Homo sapiens
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